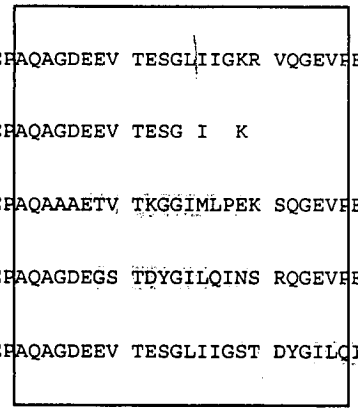
Figure 1



MSEVQQLPIR AVGEYVILVS EPAQAGDEEV TESGLIIGKR VQGEVPELCV VHSVGPDVPE GFCEVGDLTS LPVGQIRNVP HPFVALGLKQ PKEIKQKFVT CHYKAIPCLY K
T4Hsp10

MSEVQQLPIR AVGEYVILVS EPAQAGDEEV TESG I K LCV VHSVGPDVPE GFCEVGDLTS LPVGQIRNVP HPFVALGLKQ PKEIKQKFVT CHYKAIPCLY K
T4Hsp10d8C

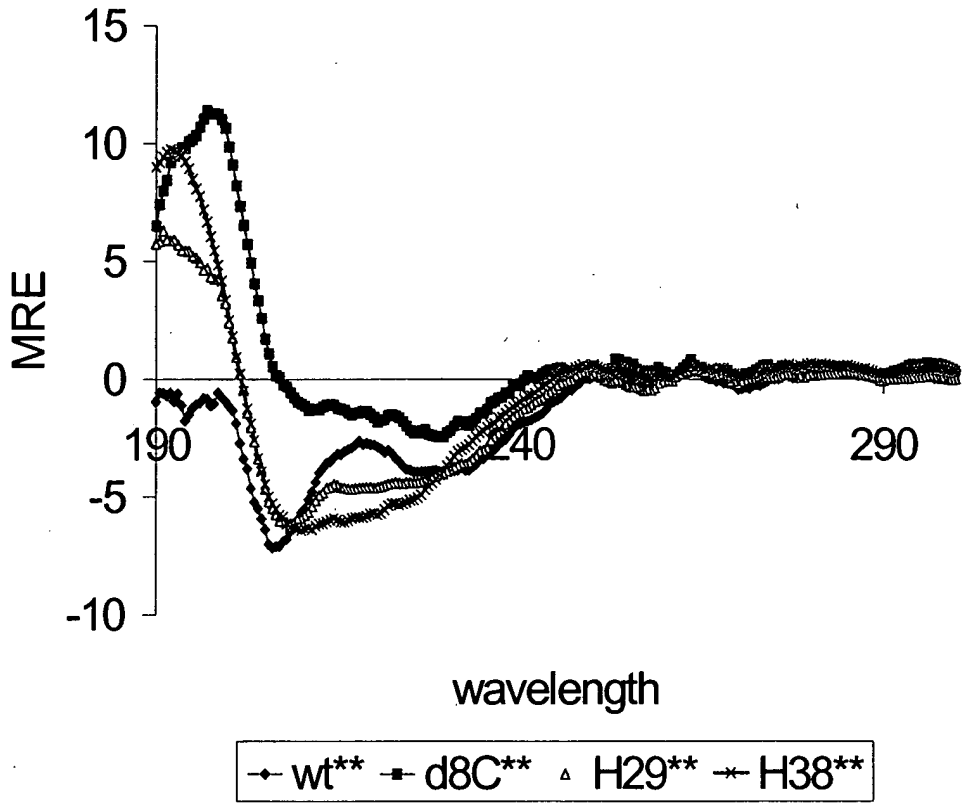
MSEVQQLPIR AVGEYVILVS EPAQAAAETV TKGGIMLPEK SQGEVPELCV VHSVGPDVPE GFCEVGDLTS LPVGQIRNVP HPFVALGLKQ PKEIKQKFVT CHYKAIPCLY K
T4Hsp10mml

MSEVQQLPIR AVGEYVILVS EPAQAGDEGS TDYGILQINS RQGEVPELCV VHSVGPDVPE GFCEVGDLTS LPVGQIRNVP HPFVALGLKQ PKEIKQKFVT CHYKAIPCLY K
T4Hsp10HEL29

MSEVQQLPIR AVGEYVILVS EPAQAGDEEV TESGLIIGST DYGILQINSR VHSVGPDVPE GFCEVGDLTS LPVGQIRNVP HPFVALGLKQ PKEIKQKFVT CHYKAIPCLY K
T4Hsp10HEL38

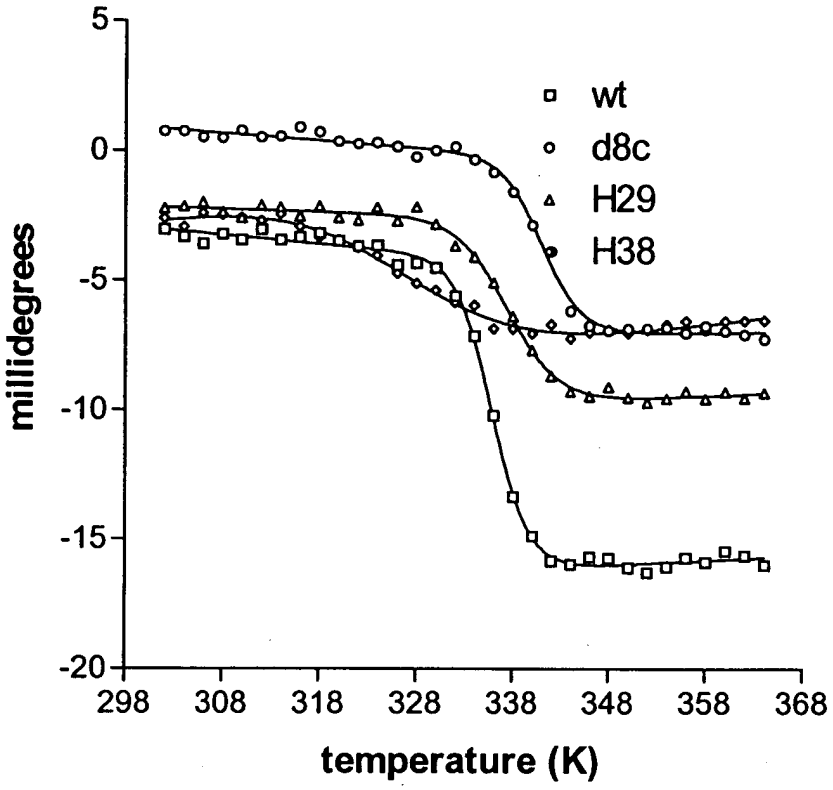
Highlighted sequences correspond to the "unstable polypeptide segments" that restore proteolytic sensitivity in the mobile loop.

EXHIBIT D



WT: T4Hsp10
d8C: T4Hsp10d8C
Hel29: T4Hsp10Hel29
Hel38: T4Hsp10Hel38

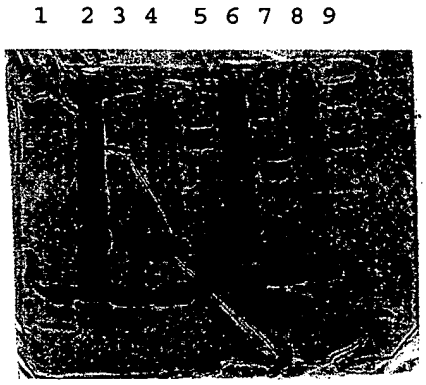
Figure 2



WT: T4Hsp10
d8C: T4Hsp10d8C
Hel29: T4Hsp10Hel29
Hel38: T4Hsp10Hel38

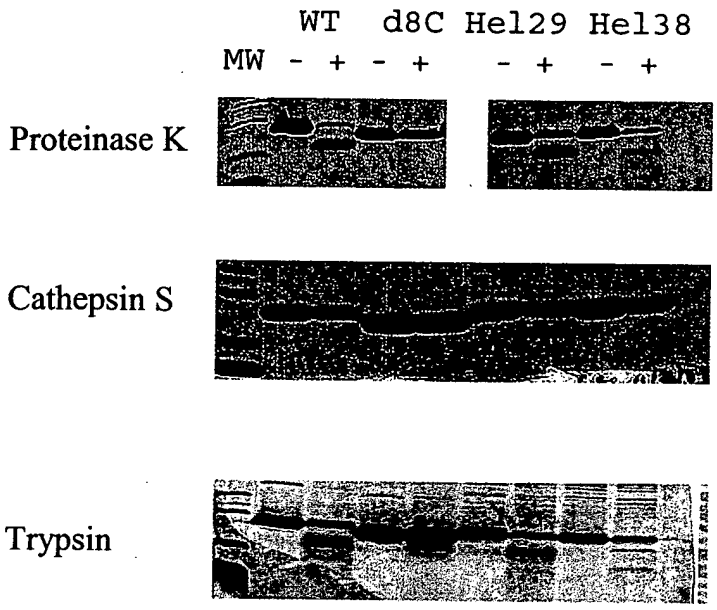
Figure 3

Figure 4.



Lane 1. T4Hsp10 – no glutaraldehyde
Lane 2. T4Hsp10 – glutaraldehyde
Lane 3. T4Hsp10d8C – no glutaraldehyde
Lane 4. T4Hsp10d8C – glutaraldehyde
Lane 5. T4Hsp10Hel29 – no glutaraldehyde
Lane 6. T4Hsp10Hel29 – glutaraldehyde
Lane 7. T4Hsp10Hel38 – no glutaraldehyde
Lane 8. T4Hsp10Hel38 – glutaraldehyde
Lane 9. Molecular weight markers

Figure 5



WT: T4Hsp10
d8C: T4Hsp10d8C
Hel29: T4Hsp10Hel29
Hel38: T4Hsp10Hel38
+ enzyme present
- enzyme absent

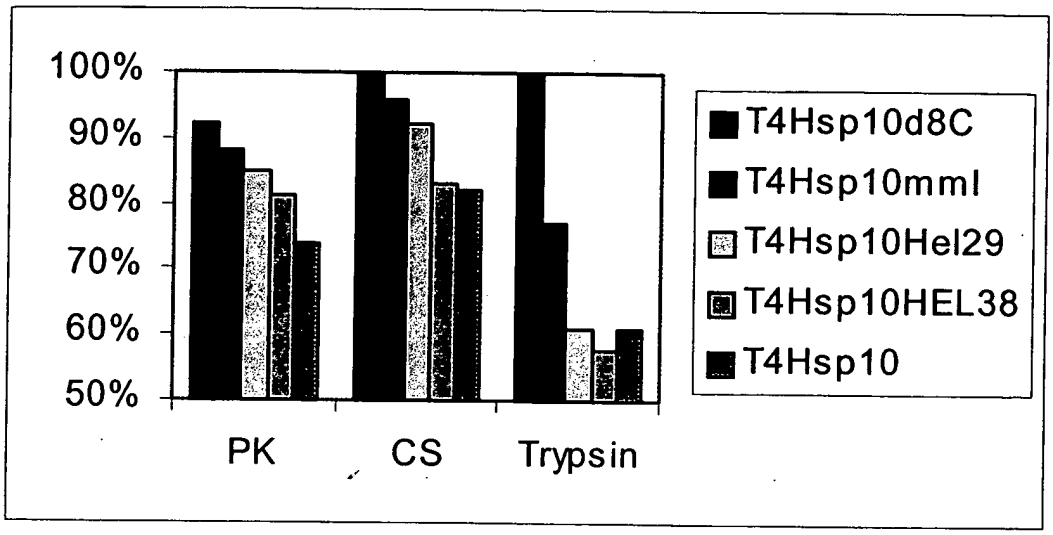

Percent intact protein remaining after proteolysis
100%
90%
80%
70%
60%
50%
PK
CS
Trypsin
T4Hsp10d8C
T4Hsp10mml
T4Hsp10Hel29
T4Hsp10HEL38
T4Hsp10

Figure 6